

SEQUENCE LISTING

<110> MINOPRIO, PAOLA

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<120> CLONING, SEQUENCING, AND EXPRESSION OF A GENE ENCODING
AN EUKARYOTIC AMINO ACID RACEMASE, AND DIAGNOSTIC,
THERAPEUTIC, AND VACCINATION APPLICATIONS OF PARASITE
AND VIRAL MITOGENS

<130> 03495.0200

<140> 09/725,945

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<160> 26

-<170>-PatentIn Ver. 2.1

<210> 1

<211> 418

<212> PRT

<213> Trypanosoma cruzi

<400> 1

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Gln Glu Lys Leu Leu Phe Asp Gln Lys Tyr Lys Ile Ile Lys Gly Glu

35 40 45

Lys Lys Glu Lys Lys Asn Gln Arg Ala Asn Arg Arg Glu His Gln

50 55 60

Gln Lys Arg Glu Ile Met Arg Phe Lys Ser Phe Thr Cys Ile Asp

65 70 75 80

Met His Thr Glu Gly Glu Ala Ala Arg Ile Val Thr Ser Gly Leu Pro

85 90 95

His Ile Pro Gly Ser Asn Met Ala Glu Lys Lys Ala Tyr Leu Gln Glu

100 105 110

Asn Met Asp Tyr Leu Arg Arg Gly Ile Met Leu Glu Pro Arg Gly His

115 120 125

Asp Asp Met Phe Gly Ala Phe Leu Phe Asp Pro Ile Glu Glu Gly Ala

130 135 140

Asp Leu Gly Met Val Phe Met Asp Thr Gly Gly Tyr Leu Asn Met Cys

145 150 155 160

Gly His Asn Ser Ile Ala Ala Val Thr Ala Ala Val Glu Thr Ile

165 170 175

Val Ser Val Pro Ala Lys Ala Thr Asn Val Pro Val Val Leu Asp Thr

180 185 190

Pro Ala Gly Leu Val Arg Gly Thr Ala His Leu Gln Ser Gly Thr Glu

195 200 205

Ser Glu Val Ser Asn Ala Ser Ile Ile Asn Val Pro Ser Phe Leu Tyr

210 215 220

Gln Gln Asp Val Val Val Leu Pro Lys Pro Tyr Gly Glu Val Arg

225 230 235 240

Val Asp Ile Ala Phe Gly Gly Asn Phe Phe Ala Ile Val Pro Ala Glu

245 250 255

Gln Leu Gly Ile Asp Ile Ser Val Gln Asn Leu Ser Arg Leu Gln Glu

260 265 270

Ala Gly Glu Leu Leu Arg Thr Glu Ile Asn Arg Ser Val Lys Val Gln

275 280 285

His Pro Gln Leu Pro His Ile Asn Thr Val Asp Cys Val Glu Ile Tyr

290 295 300

Gly Pro Pro Thr Asn Pro Glu Ala Asn Tyr Lys Asn Val Val Ile Phe

305 310 315 320

Gly Asn Arg Gln Ala Asp Arg Gly Thr Ser Ala Lys Met Ala Thr Leu

325 330 335

Tyr Ala Lys Gly Gln Leu Arg Ile Gly Glu Thr Phe Val Tyr Glu Ser

340 345 350

Ile Leu Gly Ser Leu Phe Gln Gly Arg Val Leu Gly Glu Glu Arg Ile

355 360 365

Pro Gly Val Lys Val Pro Val Thr Lys Asp Ala Glu Glu Gly Met Leu

370 375 380

Val Val Thr Ala Glu Ile Thr Gly Lys Ala Phe Ile Met Gly Phe Asn

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405 410 415

Lys Gln

<210> 2

<211> 389

<212> PRT

<213> Trypanosoma cruzi

<400> 2

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20 25 30

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35 40 45

Cys Ile Asp Met His Thr Glu Gly Glu Ala Ala Arg Ile Val Thr Ser

50 55 60

Gly Leu Pro His Ile Pro Gly Ser Asn Met Ala Glu Lys Lys Ala Tyr

65 70 75 80

Leu Gln Glu Asn Met Asp Tyr Leu Arg Arg Gly Ile Met Leu Glu Pro

85 90 95

Arg Gly His Asp Asp Met Phe Gly Ala Phe Leu Phe Asp Pro Ile Glu

100 105 110

Glu Gly Ala Asp Leu Gly Met Val Phe Met Asp Thr Gly Gly Tyr Leu

115 120 125

Asn Met Cys Gly His Asn Ser Ile Ala Ala Val Thr Ala Ala Val Glu

130 135 140

Thr Gly Ile Val Ser Val Pro Ala Lys Ala Thr Asn Val Pro Val Val

145 150 155 160

Leu Asp Thr Pro Ala Gly Leu Val Arg Gly Thr Ala His Leu Gln Ser

165 170 175

Gly Thr Glu Ser Glu Val Ser Asn Ala Ser Ile Ile Asn Val Pro Ser

180 185 190

Phe Leu Tyr Gln Gln Asp Val Val Val Val Leu Pro Lys Pro Tyr Gly

195 200 205

Glu Val Arg Val Asp Ile Ala Phe Gly Gly Asn Phe Phe Ala Ile Val

210 215 220

Pro Ala Glu Gln Leu Gly Ile Asp Ile Ser Val Gln Asn Leu Ser Arg

225 230 235 240

Leu Gln Glu Ala Gly Glu Leu Leu Arg Thr Glu Ile Asn Arg Ser Val

245 250 255

Lys Val Gln His Pro Gln Leu Pro His Ile Asn Thr Val Asp Cys Val

260 265 270

Glu Ile Tyr Gly Pro Pro Thr Asn Pro Glu Ala Asn Tyr Lys Asn Val

275 280 285

Val Ile Phe Gly Asn Arg Gln Ala Asp Arg Gly Thr Ser Ala Lys Met

290 295 300

Ala Thr Leu Tyr Ala Lys Gly Gln Leu Arg Ile Gly Glu Thr Phe Val

305 310 315 320

Tyr Glu Ser Ile Leu Gly Ser Leu Phe Gln Gly Arg Val Leu Gly Glu

325 330 335

Glu Arg Ile Pro Gly Val Lys Val Pro Val Thr Lys Asp Ala Glu Glu

340 345 350

Gly Met Leu Val Val Thr Ala Glu Ile Thr Gly Lys Ala Phe Ile Met

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Phe Thr Leu Lys Gln

385

<210> 3

<211> 29

<212> PRT

<213> Trypanosoma cruzi

<400> 3

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<210> 4

<211> 354

<212> PRT

<213> Trypanosoma cruzi

<400> 4

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Asn Met Ala Glu Lys Lys Ala Tyr Leu Gln Glu Asn Met Asp Tyr Leu

35 40 45

Arg Arg Gly Ile Met Leu Glu Pro Arg Gly His Asp Asp Met Phe Gly

50 55 60

Ala Phe Leu Phe Asp Pro Ile Glu Glu Gly Ala Asp Leu Gly Met Val

65 70 75 80

Phe Met Asp Thr Gly Gly Tyr Leu Asn Met Cys Gly His Asn Ser Ile

85 90 95

Ala Ala Val Thr Ala Ala Val Glu Thr Gly Ile Val Ser Val Pro Ala

100 105 110

Lys Ala Thr Asn Val Pro Val Val Leu Asp Thr Pro Ala Gly Leu Val

115 120 125

Arg Gly Thr Ala His Leu Gln Ser Gly Thr Glu Ser Glu Val Ser Asn

130 135 140

Ala Ser Ile Ile Asn Val Pro Ser Phe Leu Tyr Gln Gln Asp Val Val

145 150 155 160

Val Val Leu Pro Lys Pro Tyr Gly Glu Val Arg Val Asp Ile Ala Phe

165 170 175

Gly Gly Asn Phe Phe Ala Ile Val Pro Ala Glu Gln Leu Gly Ile Asp

180 185 190

Ile Ser Val Gln Asn Leu Ser Arg Leu Gln Glu Ala Gly Glu Leu Leu

195 200 205

Arg Thr Glu Ile Asn Arg Ser Val Lys Val Gln His Pro Gln Leu Pro

210 215 220

His Ile Asn Thr Val Asp Cys Val Glu Ile Tyr Gly Pro Pro Thr Asn

225 230 235 240

Pro Glu Ala Asn Tyr Lys Asn Val Val Ile Phe Gly Asn Arg Gln Ala

245 250 255

Asp Arg Ser Pro Cys Gly Thr Gly Thr Ser Ala Lys Met Ala Thr Leu

260 265 270

Tyr Ala Lys Gly Gln Leu Arg Ile Gly Glu Thr Phe Val Tyr Glu Ser

275 280 285

Ile Leu Gly Ser Leu Phe Gln Gly Arg Val Leu Gly Glu Glu Arg Ile

290 295 300

Pro Gly Val Lys Val Pro Val Thr Lys Asp Ala Glu Glu Gly Met Leu

305 310 315 320

Val Val Thr Ala Glu Ile Thr Gly Lys Ala Phe Ile Met Gly Phe Asn

325 330 335

Thr Met Leu Phe Asp Pro Thr Asp Pro Phe Lys Asn Gly Phe Thr Leu

340 345 350

Lys Gln

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<211> 330

<212> PRT

<213> Clostridium sticklandii

<400> 5

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Thr Met Ala Asp Lys Lys Lys Tyr Leu Glu Asp Asn Leu Asp Tyr Val
35 40 45

Arg Thr Ala Leu Met His Glu Pro Arg Gly His Asn Asp Met Phe Gly
50 55 60

Ser Ile Ile Thr Ser Ser Asn Asn Lys Glu Ala Asp Phe Gly Ile Ile
65 70 75 80

Phe Met Asp Gly Gly Gly Tyr Leu Asn Met Cys Gly His Gly Ser Ile
85 90 95

Gly Ala Ala Thr Val Ala Val Glu Thr Gly Met Val Glu Met Val Glu
100 105 110

Pro Val Thr Asn Ile Asn Met Glu Ala Pro Ala Gly Leu Ile Lys Ala
115 120 125

Lys Val Met Val Glu Asn Glu Lys Val Lys Glu Val Ser Ile Thr Asn
130 135 140

Val Pro Ser Phe Leu Tyr Met Glu Asp Ala Lys Leu Glu Val Pro Ser
145 150 155 160

Leu Asn Lys Thr Ile Thr Phe Asp Ile Ser Phe Gly Gly Ser Phe Phe
165 170 175

Ala Ile Ile His Ala Lys Glu Leu Gly Val Lys Val Glu Thr Ser Gln

180 185 190

Val Asp Val Leu Lys Lys Leu Gly Ile Glu Ile Arg Asp Leu Ile Asn

195 200 205

Glu Lys Ile Lys Val Gln His Pro Glu Leu Glu His Ile Lys Thr Val

210 215 220

Asp Leu Val Glu Ile Tyr Asp Glu Pro Ser Asn Pro Glu Ala Thr Tyr

225 230 235 240

Lys Asn Val Val Ile Phe Gly Gln Gly Gln Val Asp Arg Gly Thr Ser

245 250 255

Ala Lys Leu Ala Thr Leu Tyr Lys Lys Gly His Leu Lys Ile Asp Glu

260 265 270

Lys Glu Val Tyr Glu Ser Ile Thr Gly Thr Met Phe Lys Gly Arg Val

275 280 285

Leu Glu Glu Thr Lys Val Gly Glu Phe Asp Ala Ile Ile Pro Glu Ile

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Glu Asp Pro Leu Lys Tyr Gly Phe Thr Val

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<210> 6

<211> 314

<212> PRT

<213> Pseudomonas aeruginosa

<400> 6

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Glu Arg Arg Arg Leu Leu Gly Glu Arg His Asp Ala Trp Arg Ala Ala

35 40 45

Cys Ile Leu Glu Pro Arg Gly Ser Asp Val Leu Val Gly Ala Leu Leu

50 55 60

Cys Ala Pro Val Asp Pro Glu Ala Cys Ala Gly Val Ile Phe Phe Asn

65 70 75 80

Asn Ser Gly Tyr Leu Gly Met Cys Gly His Gly Thr Ile Gly Leu Val

85 90 95

Ala Ser Leu Ala His Leu Gly Arg Ile Gly Pro Gly Val His Arg Ile

100 105 110

Glu Thr Pro Val Gly Glu Val Glu Ala Thr Leu His Glu Asp Gly Ser

115 120 125

Val Ser Val Arg Asn Val Pro Ala Tyr Arg Tyr Arg Arg Gln Val Ser

130 135 140

Val Glu Val Pro Gly Ile Gly Arg Val Ser Gly Asp Ile Ala Trp Gly

145 150 155 160

Gly Asn Trp Phe Phe Leu Val Ala Gly His Gly Gln Arg Leu Ala Gly

165 170 175

Asp Asn Leu Asp Ala Leu Thr Ala Tyr Thr Val Ala Val Gln Gln Ala

180 185 190

Leu Asp Asp Gln Asp Ile Arg Gly Glu Asp Gly Gly Ala Ile Asp His

195 200 205

Ile Glu Leu Phe Ala Asp Asp Pro His Ala Asp Ser Arg Asn Phe Val

210 215 220

Leu Cys Pro Gly Lys Ala Tyr Asp Arg Ser Pro Cys Gly Thr Gly Thr

225 230 235 240

Ser Ala Lys Leu Ala Cys Leu Ala Ala Asp Gly Lys Leu Leu Pro Gly

245 250 255

Gln Pro Trp Arg Gln Ala Ser Val Ile Gly Ser Gln Phe Glu Gly Arg

260 265 270

Tyr Glu Trp Leu Asp Gly Gln Pro Gly Gly Pro Ile Val Pro Thr Ile

275 280 285

Arg Gly Arg Ala His Val Ser Ala Glu Ala Thr Leu Leu Leu Ala Asp

290 295 300

Asp Asp Pro Phe Ala Trp Gly Ile Arg Arg

305 310

<210> 7

<211> 1665

<212> DNA

<213> Trypanosoma cruzi

<400> 7

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tgtgtgttc ccttgatctc tcgaacaggg cagaaaaagc ttctgttga ccaaaaatat 180
aaaattatta agggcgagaa aaaagaaaaag aaaaaaaaaatc aacgagaaaa caggagagaa 240
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tggTccacc ggtcgccggcg gggTctgtg ggtggaggag tcctaaatcc cgcacccctgg 1620
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<210> 8

<211> 1575

<212> DNA

<213> Trypanosoma cruzi

<400> 8

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cctgcgggt tggTgcgcgg tacggcacac cttcagagtg gtactgagag tgaggtgtca 600
aatgcgagta ttatcaatgt accctcattt ttgtatcagc aggtgtggt ggtgtgtt 660

<210> 9

<211> 1524

<212> DNA

<213> Trypanosoma cruzi

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1524

<210> 10

<211> 87

<212> DNA

<213> Trypanosoma cruzi

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ttttttgtg tgttccctt gatctct

87

<210> 11

<211> 1395

<212> DNA

<213> Trypanosoma cruzi

<400> 11

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ggtggaggag tcctaaatcc cgcacctcg aggaataaac atattcaat ttcatatctt 1380
ggaatcaaaa ggcac 1395

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<220>

<221> modified_base

<222> (1)..(20)

<223> "n" represents inosine

<400> 12

ttnccraada tnacnacgtt 20

<210> 13

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<220>

<221> modified_base
<222> (1)..(21)
<223> "n" represents inosine

<400> 13
athgcnttyg gnggnaaytt t 21

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
<222> (1)..(20)
<223> "n" represents inosine

<400> 14
tnccraada tnacnacgtt 20

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 15

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<210> 16

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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<210> 17

<211> 1665

<212> DNA

<213> Trypanosoma cruzi

<400> 17

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tgtgtgttcc ctttgatctc tcgaacaggg cagaaaaagc ttctgttga ccaaaaatat 180

aaaattatta agggcgagaa aaaagaaaag aaaaaaaaaatc aacgagcaaa caggagagaa 240

caccaacaaa aaagggaaat tatgcgatt aagaaatcat tcacatgcat cgacatgcat 300

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atggcggaga agaaaagcata cctgcaggaa aacatggatt atttgaggcg tggcataatg 420
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